



Ce orf1 -----
Dm orf1 MSPNRWILL IFYISYLMFC AAIYYHIEHG EEKISRAEQR KAQIAINEYL 50
Consensus 50

Ce orf1 ----- --MSDQLFVA FEKYFLTSNE VKKNAATETW TFSSIFFAV 38
Dm orf1 LEELGDKNTT TQDEILQRIS DYCDKPVTLPT PTYDDTPYTW TRYHARFFAF 100
Consensus TW TF... FFA 100
(SEQ ID NO: 65)

Ce orf1 TVVTTIGYGN PVFVNIIGRI WCILFSLIGI PLTLVTIACL AGKFLSEHLV 88
Dm orf1 TVCSTIGYGN ISPTIFAGRM IMIAYSVIGI PVNGILFACL ----- 140
Consensus TV...T...GYGN...P...V...NI...GR...I...S...GI...E...A...L... 150
(SEQ ID NO: 66)

Ce orf1 WLYGNLKLK YLILSRHKE RREHVCECH SHGMCHDMI EKKIPAFLV 138
Dm orf1 ---GEYFGRT FEAIYRRYKK YKMSTDMHYV PPQLCLITTV VIALIPGIAL 187
Consensus ...G...Y... ..R...K... ..H... ..C... ..IP... 200

Ce orf1 LAILLIVYTAF GGVLMKLEP WSFFTSHYAS FIMTTMGFG DLMRRDGYM 188
Dm orf1 FLVLPVGVH LLRELGLSS- ---ISLYAS YVTTITIGFG DYVPE-PCAN 231
Consensus ...L... ..S...Y...S... ..T...T...GFG...D...E...G... 250
(SEQ ID NO: 67)

Ce orf1 YIILLYIILG KFSMKKKQKF KIFLGLAITT MCIDLVMGY IRKIHYFGRK 238
Dm orf1 QPKEFGGWV VYQIFVIVWF IFSLOGLVMI MTFITRGLQS KKLAYLEQQL 281
ConsensusF...LG... ..M... ..G...Q... 300

Ce orf1 IQDARSALAV VGGKVLVSE LYANLMOKRA RNSREAFIV ENLYVSKHII 288
Dm orf1 SSNLKATQNR IWSGVTKDVG YLRRMLNELY ILKVKPVYTD VDIAYTLPRS 331
ConsensusV... .. 350

Ce orf1 PFIFTDIRCI -RYIDQTADA ATISTSSSAI DMQSCRFCBS RYSLNRAFKK 337
Dm orf1 NSCFPLSMYR VEPAPIPSRK RARVCADMV GPQREAGMVH ANSDTLTKL 381
Consensus ...E... ..S... ..C... ..S... ..K... 400

Ce orf1 ----- 337
Dm orf1 DREKTFETAE AYHQTTDLLA KVVNALATVK PPPAEQEDAA LYGGYHGFSD 431
Consensus 450

Ce orf1 ----- 337 (SEQ ID NO: 39)
Dm orf1 SQILASEWSF STVNEFTSPR RPRARACSDF NLEAPRWQSE RPLRSSHNEW 481 (SEQ ID NO: 37)
Consensus 500

FIG. 4